

CLAIMS

We claim:

1. A Novel DNA sequences expressed and repressed during winter dormancy in the apical buds of *Camellia sinensis* L. (O.) Kuntze (tea) bush or a tree species, said sequences comprising sequence ID 1 to 4 as shown here below:

SEQ ID NO:1

5'- ATCGCCGTAA TTGCCATGTT TTCCCTCTCA CCGGAATCCT ACG
TTATCC CCTTACCTTC GTGAACATTA CAGTAGGAAT CCGTGGTCCA
ATTATCAACT TAATTTTGGG CGCATCTGTT CGTGTTAACT AGAAGCCATG
TATACATACA ATACAACATG GTTCACTCCT CCTACAGATT ATGAGTTGAA
CTTTTATAAT AAGTTGTAAT AATGGCTTCT GAATAAGGAG AAGAGGAGCC
TCTGTTTGTGTT TTACTIONTATTA CAGATGTGAT ATCGTTCAAC AACTTTGATT
CTGCGAAAAA AAAAA-3'

SEQ ID NO: 2

5'- AGAAGTACCT GAAAGGAAGC TTAACGAGGT GAACATCCAT
TGCAGCCAGC CCTGGAATCT GTACAGGGCA ACTCTGAACC GGAATTATTT
TAATAACCCG TGGGCAATGA TTGCAATTAT GGCTCGTTTG GTATTACTTC
TACTCACTTA GACACAACCTG TATTTACGGT TTTCGCTGGA ATTGTAATTG
TTGGAGCGAC AAAATAGATG GTCACAACCTT ATTGGTGAGA GTATCAGTGT
GCTCTTCTTT ATCGTCTTTA ACTCTCCGTG GTAATTACTT TGACAATATT
CATACAT -3'

SEQ ID NO: 3

5'- GAGACTCAGC TCAGCAATCA TGTCTAAGT GAATGTCACT CTATCGCCTT
CTTGTCCTTC TTAGACATAC TACATCCTCA TTCTGCTAGA AATGAACTCA
TGTAGGTTTT GAAGTTGGGA ACTTTTGAAA CTGTGTTGTT TGGGTGCTGT
CTGTTATACA ATTCTCTCAA CTGCGGAGAA TTGACGTTGG TTGTAGTGGA
ATTCAACACT TGGGTTTTGT TCTTAGTTAA AAAAAAAAAA-3'

SEQ ID NO: 4

5'-ATAGCTTAGT CACGTGTCTC TTGAGAATGG ACTACGTAGT TGTAAAGTTG
GGTGATCAGA AGGCGTTGAT GATGAATGTA TGAAGCAGAG ACTACTGAAT
GTAATTTTGT TGTTGAAAGA TGAATGATTT ATTAATGCCT GCATATCTTT
CTATTGTTTG ATGCCAAACC TTTGGGCACA TTTTCTTT CTTTTGTGA
TAATGTTCTC TTCTTGCAAA AAAAAAAA-3'

2. The Novel DNA sequences as claimed in claim 1 which are cloned from the tea bush of the same genetic make up.

3. The Novel DNA sequences as claimed in claim 1 which are cloned from the tea bush of the same genetic make up growing under field conditions.

4. Novel DNA sequences as claimed in claim 1, are associated with winter dormancy in tea.

5. Method to clone Novel DNA sequences as claimed in claim 1 from the tree species tea of the same genetic make up growing under field conditions.

6. Novel DNA sequences as claimed in claim 1, which are cloned by any methods but not limited to, subtractive hybridization and differential screening.

7. Novel DNA sequences as claimed in claim 1 wherein, the nucleotide sequence of the DNA is given in SEQ ID NO: 1.

8. Novel DNA sequences as claimed in claim 7 with the nucleotide sequence of the DNA as is given in SEQ ID NO: 1 is overexpressed only in non-dormant apical buds of tea.

9. Novel DNA sequences as claimed in claim 1 wherein, the nucleotide sequence of the DNA is given in SEQ ID NO:2

10. Novel DNA sequences as claimed in claim 9 with the nucleotide sequence of the DNA as is given in SEQ ID NO: 2 is expressed only in non-dormant apical buds of tea.

11. Novel DNA sequences as claimed in claim 1 wherein the nucleotide sequence of the DNA is given in SEQ ID NO: 3

12. Novel DNA sequences as claimed in claim 11 with the nucleotide sequence of the DNA as is given in SEQ ID NO:3 is expressed only in non-dormant apical buds of tea.

13. Novel DNA sequences as claimed in claim 1 wherein, the nucleotide sequence of the DNA is given in SEQ ID NO: 4

14. Novel DNA sequences as claimed in claim 13 with the nucleotide sequence of the DNA as is given in SEQ ID NO: 4 is expressed only in dormant apical buds of tea.

15. Novel sequences as claimed in claim 1 which are capable of being cloned to

full-length cDNA.

16. Novel sequences as claimed in claim 1, which are capable of being cloned to full length genomic DNA.

17. Novel sequences as claimed in claim 1, which are capable of being cloned to important sequences, such as but not limited to, promoter sequences and regulatory sequences etc.,

18. Use of sequence data as claimed in claim 1, important information on the gene regulation can be obtained.

19. Use of genes as claimed in claim 1, wherein it is possible to modulate winter dormancy in plants after transferring these genes using the techniques such as, but not limited to, *Agrobacterium* mediated transformation and Bialistic medited transformation

20. Use of genes as claimed in claim 1, wherein it is possible to modulate winter dormancy in the plants such as, but not limited to, tea, plums, cherries, peaches, *Taxus*, apples, peers, vines, grapes, olives, Kiwi fruit, figs, morus, strawberries, raspberries, cranberies, blackberries, loganberries, almonds, walnuts and chestnuts after transferring these genes using the techniques such as , but not limited to, *Agrobacterium* mediated transformation and bialistic medited transformation.

21. Use of sequence data as claimed in claim 1, wherein important information on the gene regulation can be obtained to be exploited to regulate gene expression in transgene.

22. Use of cDNAs and the genomic DNAs as claimed in claims 15-16, for synthesizing unique proteins.

23. Use of unique proteins as claimed in claim 22 for raising antibodies.

24. Use of antibodies as claimed in claim 23, as probe to look for the similar proteins in other plants, animal and/or microbial systems or the like.

25. Use of novel sequences as claimed in claim 1 and cDNAs and the genomic

DNAs as claimed in claims 15-16, as probe to look for the sequences of nucleotides in other plants, animal and/or microbial systems and the like.

26. Use of novel sequences as claimed in claim 1 and cDNAs and the genomic
5 DNAs as claimed in claims 15-16, as probe to look for the expression of these sequences of nucleotides in other plants, animal and/or microbial systems and the like.

27. A method to correlate the identified gene with the process of dormancy of tea buds as described for sequence ID 1 is unique.

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28. A method as claimed in claim 27 which can be applied to other sequence ID as well.

29. A method as claimed in claim 27 which can be applied to other crops such as,
15 but not limited to plums, cherries, peaches, *Taxus*, apples, peers, vines, grapes, olives, Kiwi fruit, figs, morus, strawberries, raspberries, cranberries, blackberries, loganberries, almonds, walnuts and chestnuts as well for correlating similar genes.